

[illegible]

```

ALIGNMENTS

RESULT 1
US-11-005-216-3
; Sequence 3, Application US/11005216
; Publication No. US20050287633A1
; GENERAL INFORMATION:
; APPLICANT: Mcintyre, Peter
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/11/005, 216
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US/09/533, 220
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30

```

```

/ C-LENGTH: 5155
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-005-216-3

      8.0%; Score 49.4; DB 14; Length 5155;
Query Match Best Local Similarity 83.6%; Pred.No. 0.00024;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0

QY 506 CGGTGTTCCTGAAGGCGCTATATAAGGGGGGGCGCGCTTCGTCTCATTCCTGGA 565
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 CGGTGTTCCTGAAGGCGGTATAAAGGGGTGGGGCGCGTTCGTCTCATCTCTT 626

QY 566 CCGGCTC 572
      ||| ||| |||
Db 627 CCGCATC 633

RESULT 2
US-11-077-716-1
; Sequence 1, Application US/11077716
; Publication No. US20050260180A1
; GENERAL INFORMATION:

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:20:15 ; Search time 800.831 Seconds
(without alignments)
6340.158 Million cell updates/sec

Title: US-10-781-055A-36

Perfect score: 614

Sequence: 1 cggatcatgatgtctcgat.....ctctcagtcagcgatcaa 614

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	614	7 US-10-781-055-36	Sequence 36, Appl
2	568	92.5	596	7 US-10-781-055-37	Sequence 37, Appl
3	190	30.9	190	7 US-10-781-055-35	Sequence 35, Appl
4	60	9.8	60	7 US-10-781-055-3	Sequence 3, Appl
5	51	8.3	51	7 US-10-781-055-1	Sequence 1, Appl
6	49.4	8.0	3788	3 US-09-392-462-1	Sequence 1, Appl
7	49.4	8.0	3788	3 US-09-540-991-1	Sequence 1, Appl
8	49.4	8.0	3788	6 US-10-291-041-1	Sequence 1, Appl
9	49.4	8.0	3788	7 US-10-351-603-1	Sequence 1, Appl
10	49.4	8.0	5155	5 US-10-128-853-3	Sequence 3, Appl
11	49.4	8.0	5374	5 US-10-007-357-7	Sequence 3, Appl
12	49.4	8.0	5462	5 US-10-007-357-6	Sequence 7, Appl
13	49.4	8.0	7522	8 US-10-491-121-36	Sequence 36, Appl
14	49.4	8.0	7711	7 US-10-359-120-49	Sequence 49, Appl
15	49.4	8.0	7711	8 US-10-491-121-35	Sequence 35, Appl
16	49.4	8.0	7789	7 US-10-359-120-45	Sequence 45, Appl
17	49.4	8.0	7789	7 US-10-359-120-48	Sequence 48, Appl
18	49.4	8.0	7792	7 US-10-359-120-46	Sequence 46, Appl
19	49.4	8.0	7828	7 US-10-359-120-47	Sequence 47, Appl
20	49.4	8.0	7867	7 US-10-359-120-42	Sequence 42, Appl
21	49.4	8.0	7870	7 US-10-359-120-39	Sequence 39, Appl
22	49.4	8.0	7870	7 US-10-359-120-43	Sequence 43, Appl
23	49.4	8.0	7885	7 US-10-359-120-44	Sequence 44, Appl

24	49.4	8.0	7906	7 US-10-359-120-40	Sequence 40, Appl
25	49.4	8.0	7909	7 US-10-359-120-41	Sequence 41, Appl
26	49.4	8.0	7948	7 US-10-359-120-36	Sequence 36, Appl
27	49.4	8.0	7963	7 US-10-359-120-37	Sequence 37, Appl
28	49.4	8.0	7966	7 US-10-359-120-38	Sequence 38, Appl
29	49.4	8.0	7987	7 US-10-359-120-35	Sequence 35, Appl
30	49.4	8.0	8131	8 US-10-491-121-12	Sequence 12, Appl
31	49.4	8.0	8146	8 US-10-491-121-20	Sequence 20, Appl
32	49.4	8.0	8199	8 US-10-491-121-29	Sequence 29, Appl
33	49.4	8.0	8221	8 US-10-491-121-27	Sequence 27, Appl
34	49.4	8.0	8238	3 US-09-482-682-50	Sequence 50, Appl
35	49.4	8.0	8256	8 US-10-491-121-32	Sequence 32, Appl
36	49.4	8.0	8338	8 US-10-491-121-26	Sequence 26, Appl
37	49.4	8.0	8439	8 US-10-491-121-25	Sequence 25, Appl
38	49.4	8.0	10783	8 US-10-491-121-25	Sequence 25, Appl
39	49.4	8.0	30365	7 US-10-384-136-4	Sequence 4, Appl
40	49.4	8.0	31183	7 US-10-431-598-19	Sequence 19, Appl
41	49.4	8.0	31183	8 US-10-825-282-4	Sequence 4, Appl
42	49.4	8.0	31672	7 US-10-384-136-3	Sequence 3, Appl
43	49.4	8.0	31880	7 US-10-427-717-507	Sequence 507, App
44	49.4	8.0	31976	8 US-10-766-307A-1	Sequence 1, Appl
45	49.4	8.0	31976	8 US-10-766-307A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-781-055-36
; Sequence 36, Application US/10781055
; Publication No. US20040171573A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN
; APPLICANT: QU, BAO-XI
; TITLE OF INVENTION: RATIONALLY DESIGNED AND CHEMICALLY SYNTHESIZED
; TITLE OF INVENTION: PROMOTER FOR GENETIC VACCINE AND GENE THERAPY
; FILE REFERENCE: UTSD:788US
; CURRENT APPLICATION NUMBER: US/10/781,055
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/448,166
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-781-055-36

Query Match 100.0%; Score 614; DB 7; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.6e-194; Mismatches 0; Indels 0; Gaps 0;
Matches 614; Conservative 0;

QY	1	CGGTACATGATGTTCTCGATGCAATATCACGTGAAGGTCAAAAATAGGTCAAGGTCAACCT	60
Db	1	CGGTACATGATGTTCTCGATGCAATATCACGTGAAGGTCAAAAATAGGTCAAGGTCAACCT	60
QY	61	CTCTCGGCTATCAATAAGAGTGTAGGACGGGAGAGGGGAAAAACAGAACAGACAGTG	120
Db	61	CTCTCGGCTATCAATAAGAGTGTAGGACGGGAGAGGGGAAAAACAGAACAGACAGTG	120
QY	121	CTGAGCTCAGCAGGAGTTGCCCTTTGAAAACGTTAACGTTACGTTACGTTGCGAGCTGC	180
Db	121	CTGAGCTCAGCAGGAGTTGCCCTTTGAAAACGTTAACGTTACGTTACGTTGCGAGCTGC	180
QY	181	AGCTGATTAATAATTACAGCCAAAGGCCCAAGCAAGCTTTATATGCAAAATATGCAAAAT	240
Db	181	AGCTGATTAATAATTACAGCCAAAGGCCCAAGCAAGCTTTATATGCAAAATATGCAAAAT	240
QY	241	GAGAACAGGGGGGGGGGGGCGGACATCGGTTCAACGTTTTCTGTTTCAATTTCTTCTTAT	300

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:03:35 ; Search time 164.026 Seconds
(without alignments)
6653.974 Million cell updates/sec

Title: US-10-781-055A-36

Perfect score: 614

Sequence: 1 cggatcatgatgtctcgat.....ctctcagctcagcgatcaa 614

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCITUS COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/pp COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49.4	8.0	382	2	US-08-333-706-1
2	49.4	8.0	643	2	US-08-458-372-21
3	49.4	8.0	643	8	US-09-384-327-21
4	49.4	8.0	872	2	US-08-458-372-20
5	49.4	8.0	872	8	US-09-384-327-20
6	49.4	8.0	874	9	5506118-10
7	49.4	8.0	2898	3	US-09-051-696-7
8	49.4	8.0	5155	3	US-09-533-220A-3
9	49.4	8.0	5155	3	US-10-128-853-3
10	49.4	8.0	5374	3	US-10-007-357-7
11	49.4	8.0	5462	3	US-10-007-357-6
12	49.4	8.0	6151	6	PCT-US91-02954-12
13	49.4	8.0	6306	6	PCT-US94-00658-1
14	49.4	8.0	32166	3	US-09-563-930-11
15	49.4	8.0	32798	3	US-09-604-6948-1
16	49.4	8.0	34303	2	US-08-735-609-4
17	49.4	8.0	34303	2	US-08-735-609-4
18	49.4	8.0	34303	3	US-09-315-372-4
19	49.4	8.0	34303	3	US-09-244-752-4
20	49.4	8.0	34303	3	US-09-245-497-4
21	49.4	8.0	34303	3	US-09-562-919-4
22	49.4	8.0	34382	2	US-08-374-483-6
23	49.4	8.0	34427	3	US-09-111-911-5
24	49.4	8.0	35408	3	US-08-973-334-3

25	49.4	8.0	35408	3	US-09-563-869A-3	Sequence 3, Appli
26	49.4	8.0	35408	3	US-08-549-489-3	Sequence 3, Appli
27	49.4	8.0	35871	3	US-09-956-335-2	Sequence 2, Appli
28	49.4	8.0	35935	2	US-08-735-609-1	Sequence 1, Appli
29	49.4	8.0	35935	2	US-08-735-609-1	Sequence 1, Appli
30	49.4	8.0	35935	3	US-08-379-452-43	Sequence 43, Appli
31	49.4	8.0	35935	3	US-09-315-372-1	Sequence 1, Appli
32	49.4	8.0	35935	3	US-09-244-752-1	Sequence 1, Appli
33	49.4	8.0	35935	3	US-09-245-497-1	Sequence 1, Appli
34	49.4	8.0	35935	3	US-09-409-670-43	Sequence 43, Appli
35	49.4	8.0	35935	3	US-09-562-919-1	Sequence 1, Appli
36	49.4	8.0	35935	3	US-09-782-378A-4	Sequence 4, Appli
37	49.4	8.0	35935	3	US-09-782-378A-5	Sequence 5, Appli
38	49.4	8.0	35937	3	US-09-956-335-1	Sequence 3, Appli
39	49.4	8.0	35978	3	US-09-952-060-30	Sequence 30, Appli
40	49.4	8.0	36620	3	US-09-952-060-25	Sequence 25, Appli
41	49.4	8.0	37474	3	US-09-952-060-28	Sequence 28, Appli
42	49.4	8.0	38519	3	US-09-865-022-2	Sequence 2, Appli
43	47.8	7.8	12445	3	US-08-171-389-579	Sequence 579, App
44	42	6.8	50	2	US-08-171-389-580	Sequence 580, App
45	42	6.8	50	2		

ALIGNMENTS

RESULT 1
US-08-333-706-1
; Sequence 1, Application US/08333706
; Patent No. 5612213
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; TITLE OF INVENTION: Vector and Mammalian Cell Line Having Improved
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: Fourth and Parker Streets
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,706
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/075,209
; FILING DATE: 10-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: CL-208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)420-5511
; TELEFAX: (510)428-4703
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 8.0%; Score 49.4; DB 2; Length 382;
Best Local Similarity 89.6%; Pred. No. 5.2e-06;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:52:47 ; Search time 3978.28 Seconds
(without alignments)
7221.025 Million cell updates/sec

Title: US-10-781-055A-36
Perfect score: 614
Sequence: 1 cgggtacatgatgttctcgat.....ctctcagtcctcaggatcaa 614

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:★

```
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	39.6	6.4	1201	10	CNS016BE	AL106532 Drosophil
2	38.2	6.2	1068	3	BM921844	BN921844 AGENCOURT
C 3	38	6.2	409	1	AL1857142	AL1857142 MENAAD-AL
C 4	37.8	6.2	1064	9	BZ247726	BZ247726 CH230-457
5	37.6	6.1	590	10	CZ481855	CZ481855 e04097-5p
C 6	37.6	6.1	859	10	CNS004Y	AL055406 Drosophil
7	37.4	6.1	796	7	CR412210	CR412210 CH412210
C 8	37.2	6.1	1079	9	CC230752	CC230752 CH261-114
9	36.8	6.0	568	6	CD125835	CD125835 MF1-0001U
10	36.8	6.0	827	9	BZ567513	BZ567513 pac82-164
11	36.8	6.0	984	10	CZ386907	CZ386907 ZWMBP0163
12	36.6	6.0	736	10	AG372972	AG372972 MUS muscu
C 13	36.6	6.0	757	11	CR806759	CR806759 GLOAA28D
14	36.6	6.0	794	8	DN112025	DN112025 1111185 M
C 15	36.4	5.9	499	9	BZ156401	BZ156401 CH230-347
C 16	36.4	5.9	549	10	CZ439879	CZ439879 OA_BBa008
17	36.4	5.9	1200	6	CD503874	CD503874 CDA64-G08
C 18	36.2	5.9	817	10	CZ998292	CZ998292 187615 To
C 19	36.2	5.9	914	1	AL544144	AL544144 AL544144
20	36	5.9	612	9	BH679464	BH679464 BOHW433TF
21	36	5.9	737	8	DR399051	DR399051 TRN036H1
C 22	36	5.9	924	10	CL297903	CL297903 ZWMBBB008

Q7 245 ACAGGGGGGGGGCGGACATCGGTTCAACGTTTCGGTTTCAATTTCCTTCCTATTAAAT 304

ALIGNMENTS

RESULT 1	CNS016BE	1201 bp	DNA	linear	GSS 26-JUL-1999
CNS016BE					
LOCUS					
DEFINITION					
					Drosophila melanogaster genome survey sequence T7 end of BAC
					BACN15E23 of DrosBAC library from Drosophila melanogaster (fruit
					fly), genomic survey sequence.

REVISION: AL106532.1
VERSION: AL106532.1 GI: 5622404

KEYWORDS
GSS.
Drosophila melanogaster (fruit fly)
SOURCE

ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
Gençöğür, I. (başar)

TITLE	Direct Submission
TOURNAMENT SUBMITTED (22 APR	

COMMENT: Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (DrosBAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11

FEATURES

1
2
3
4
5
6

ORIGIN

Query Mat

Best Local
Matches

•

1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:41:05 ; Search time 556.547 Seconds
(without alignments)
7352.695 Million cell updates/sec

Title: US-10-781-055A-36
Perfect score: 614
Sequence: 1 cgtacatgatgtctcgat.....ctctcagtcacgcatcaa 614

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	614	13 ADR90243	ADR90243 SP72 prom
2	568	92.5	596	13 ADR90244	ADR90244 SP72 prom
3	190	30.9	190	13 ADR90242	ADR90242 SP72 prom
4	60	9.8	60	13 ADR90218	ADR90218 CREB/ATF
5	51	8.3	51	13 ADR90216	ADR90216 Vitamin D
6	49.4	8.0	382	2 AAG79748	AAG79748 AML promo
7	49.4	8.0	382	2 AAT60502	AAT60502 Adeno maj
8	49.4	8.0	382	2 AAV62387	AAV62387 Nucleotid
9	49.4	8.0	561	1 AAN50287	AAN50287 Sequence
10	49.4	8.0	578	1 AAN50288	AAN50288 Sequence
11	49.4	8.0	642	2 AAG54210	AAG54210 BK enhanc
12	49.4	8.0	642	2 AAT5958456	AAT5958456 BK enhanc
13	49.4	8.0	642	2 AAT15956	AAT15956 BK enhanc
14	49.4	8.0	643	2 AAT95172	AAT95172 Sequence
15	49.4	8.0	824	1 AAN70083	AAN70083 Sequence
16	49.4	8.0	848	2 AAO13632	AAO13632 GMT mod
17	49.4	8.0	873	3 AAO39104	AAO39104 Plasmid p
18	49.4	8.0	874	1 AAN70082	AAN70082 Sequence
19	49.4	8.0	874	2 AAO3825	AAO3825 Improved

20	49.4	8.0	874	2	AAQ54209	AAQ54209 BK enhanc
21	49.4	8.0	874	2	AAQ58455	AAQ58455 BK enhanc
22	49.4	8.0	874	2	AAT36645	AAT36645 BK enhanc
23	49.4	8.0	874	2	AAT15955	AAT15955 BK enhanc
24	49.4	8.0	874	2	AAT43793	AAT43793 BK enhanc
25	49.4	8.0	874	2	AAT95171	AAT95171 BK enhanc
26	49.4	8.0	874	2	AAX18483	AAX18483 BK enhanc
27	49.4	8.0	874	5	AHH45120	AHH45120 BK protot
28	49.4	8.0	3788	3	AAZ93330	AAZ93330 PGZA-CAT
29	49.4	8.0	3788	5	AAD21318	AAD21318 CpG alter
30	49.4	8.0	5155	6	ADA42468	ADA42468 Human pla
31	49.4	8.0	5155	8	ACA61961	ACA61961 Mammalian
32	49.4	8.0	5365	1	AAN90646	AAN90646 Nucleotid
33	49.4	8.0	5374	3	AAC60706	AAC60706 Primers a
34	49.4	8.0	5413	1	AAN90649	AAN90649 Nucleotid
35	49.4	8.0	5462	3	AAC60707	AAC60707 Primers a
36	49.4	8.0	5518	1	AAN90647	AAN90647 Nucleotid
37	49.4	8.0	5566	1	AAN90648	AAN90648 Nucleotid
38	49.4	8.0	6149	1	AAN90645	AAN90645 Sequence
39	49.4	8.0	6151	1	AAN90644	AAN90644 Sequence
40	49.4	8.0	6151	2	AAQ05608	AAQ05608 Plasmid p
41	49.4	8.0	6151	2	AAQ03006	AAQ03006 Full leng
42	49.4	8.0	6165	2	AAQ20324	AAQ20324 Sol.rhesu
43	49.4	8.0	7316	2	AAQ04555	AAQ04555 Plasmid p
44	49.4	8.0	7377	2	AAQ05607	AAQ05607 Plasmid p
45	49.4	8.0	7377	2	AAQ03005	AAQ03005 Full leng

ALIGNMENTS

RESULT 1
ADR90243
ID ADR90243 standard; DNA; 614 BP.
XX
AC ADR90243;
XX
DT 18-NOV-2004 (first entry)
XX
DE SP72 promoter DNA #2.
XX
KW Promoter/enhancer; cancer; infectious disease; inflammatory disease;
KW tuberculosis; hepatitis B; HIV-1; influenza; malaria; cytostatic;
KW vaccine; gene therapy; SP72 promoter; ds.
XX
OS Unidentified.
XX
PN US2004171573-A1.
XX
PD 02-SEP-2004.
XX
PP 18-FEB-2004; 2004US-00781055.
XX
PR 18-FEB-2003; 2003US-0448166P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Johnston S, Qu B;
XX
DR WPI; 2004-634560/61.
XX
PT New nucleic acid segment comprises SP72 synthetic promoter/enhancer,
PT useful as a vaccine for genetic immunization or for gene therapy for
PT treating or preventing cancers, infectious diseases, or inflammatory
PT diseases.
XX
PS Claim 13; SEQ ID NO 36; 34pp; English.
XX
CC The present invention provides nucleic acid segments comprising a
CC synthetic promoter/enhancer or its complement. The invention is useful
CC for treating or preventing diseases or conditions including cancers,
CC infectious diseases and inflammatory diseases such as viral and parasitic
CC including tuberculosis, hepatitis B, HIV-1, influenza and malaria. The

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:46:12 ; Search time 3344.55 Seconds
(without alignments)
10435.462 Million cell updates/sec

Title: US-10-781-055A-36

Perfect score: 614

Sequence: 1 cggatcatgatgttctcgat.....ctctcagtcacgcatcaaa 614

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_ln.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_hcg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	8.0	382	6	I36987 Sequence 1
2	49.4	8.0	560	6	I02395 Sequence 1
3	49.4	8.0	578	6	I02396 Sequence 2
4	49.4	8.0	642	6	E01427 DNA sequence
5	49.4	8.0	642	6	E59622 Human prote
6	49.4	8.0	642	6	I05120 Sequence 11
7	49.4	8.0	642	6	BD014699 Recombina
8	49.4	8.0	643	6	I71451 Sequence 21
9	49.4	8.0	872	6	I71450 Sequence 20
10	49.4	8.0	874	6	E01426 DNA sequenc
11	49.4	8.0	874	6	E59621 Human prote
12	49.4	8.0	874	6	I05111 Sequence 10
13	49.4	8.0	874	6	I07642 Sequence 11
14	49.4	8.0	874	6	AR365523 Sequence
15	49.4	8.0	874	6	BD014698 Recombina
16	49.4	8.0	2898	6	AR178237 Sequence
17	49.4	8.0	3788	6	BD223711 Methylati
18	49.4	8.0	3788	6	AX282868 Sequence

19 49.4 8.0 5155 6 AR214348 Sequence
20 49.4 8.0 5155 6 AR654117 Sequence
21 49.4 8.0 5365 6 I09267 Sequence 34
22 49.4 8.0 5374 6 BD247396 Primer-as
23 49.4 8.0 5374 6 AR533276 Sequence 37
24 49.4 8.0 5413 6 I09270 Sequence 17
25 49.4 8.0 5462 6 BD247395 Sequence
26 49.4 8.0 5462 6 AR533275 Sequence 35
27 49.4 8.0 5518 6 I09268 Sequence 35
28 49.4 8.0 5566 6 I09269 Sequence 36
29 49.4 8.0 6149 6 I09252 Sequence 19
30 49.4 8.0 6151 6 I09251 Sequence 18
31 49.4 8.0 7069 11 U02442 Cloning vec
32 49.4 8.0 7711 6 AX427811 Sequence
33 49.4 8.0 7789 6 AX427807 Sequence
34 49.4 8.0 7789 6 AX427810 Sequence
35 49.4 8.0 7792 6 AX427808 Sequence
36 49.4 8.0 7819 6 CS078969 Sequence
37 49.4 8.0 7828 6 AX427809 Sequence
38 49.4 8.0 7841 6 CS078964 Sequence
39 49.4 8.0 7844 6 CS078966 Sequence
40 49.4 8.0 7852 6 CS078967 Sequence
41 49.4 8.0 7867 6 AX427804 Sequence
42 49.4 8.0 7870 6 AX427801 Sequence
43 49.4 8.0 7870 6 AX427805 Sequence
44 49.4 8.0 7885 6 AX427806 Sequence
45 49.4 8.0 7906 6 AX427802 Sequence

ALIGNMENTS

RESULT 1
I36987
LOCUS I36987 Sequence 1 from patent US 5612213.
DEFINITION I36987
ACCESSION I36987
VERSION I36987.1 GI:2084947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 382)
AUTHORS Chan,S.Y.
TITLE Method of selecting mammalian cell lines having improved productivity
JOURNAL Patent: US 5612213-A 1 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..382
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 8.0%; Score 49.4; DB 6; Length 382;
Best Local Similarity 83.6%; Pred. No. 0.0016;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 506 CCGGTGTTCTCGAAGGGCGCTATATAAGGGGGGGGGCGGTTCCTCATCTGGA 565
Db 197 CCGGTGTTCTCGAAGGGGGGCTATAAAGGGGGTGGGGGGCGGTTCCTCATCTCTT 256
Qy 566 CCGCGTC 572
Db 257 CCGCATC 263
RESULT 2
I02395
LOCUS I02395 560 bp ss-DNA linear PAT 18-MAY-1993
DEFINITION Sequence 1 from Patent US 4510245.
ACCESSION I02395
VERSION I02395.1 GI:268039
KEYWORDS

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 28, 2006, 06:24:40 ; Search time 235.464 Seconds
(without alignments)
3216.574 Million cell updates/sec

Title: US-10-781-055A-35
Perfect score: 190
Sequence: 1 aaatgacatagaaactga.....ctctcagtcctcagcgatcaa 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9258654 seqs, 1993127192 residues

Total number of hits satisfying chosen parameters: 18517308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA_New.*
- 1: /SID55/ptodata/1/pubpna/US08_NEW_PUB.seq.*
 - 2: /SID55/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 3: /SID55/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 4: /SID55/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 5: /SID55/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 6: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 7: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 8: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 9: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 10: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 11: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq.*
 - 12: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq.*
 - 13: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq.*
 - 14: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq.*
 - 15: /SID55/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	49.4	26.0	5155	14	US-11-005-216-3
2	49.4	26.0	33014	14	US-11-077-716-1
3	49.4	26.0	33592	11	US-11-249-873-1
4	49.4	26.0	33699	11	US-11-249-873-3
5	49.4	26.0	33699	11	US-11-249-873-3
6	49.4	26.0	33988	11	US-11-249-873-14
7	49.4	26.0	34341	11	US-11-249-873-2
8	49.4	26.0	34448	11	US-11-249-873-4
9	49.4	26.0	34555	8	US-10-623-155-479
10	49.4	26.0	34737	11	US-11-249-873-15
11	49.4	26.0	35696	8	US-10-860-436-1
12	49.4	26.0	35724	11	US-11-249-873-13
13	49.4	26.0	35893	8	US-10-860-436-2
14	49.4	26.0	35935	14	US-11-127-832-4
15	49.4	26.0	35937	14	US-11-127-832-5
16	49.4	26.0	36114	11	US-11-249-873-16
17	47.8	25.2	12445	9	US-10-948-344-2
18	35	18.4	35100	14	US-11-127-832-26

19	34.2	18.0	191684	14	US-11-121-086-2	Sequence 2, Appli
20	31.8	16.7	3608	11	US-11-245-147-234	Sequence 234, App
c 21	31.2	16.4	578	9	US-10-301-480-28773	Sequence 28773, A
c 22	31.2	16.4	578	10	US-10-301-480-642182	Sequence 642182,
c 23	31	16.3	48174	9	US-10-330-773-10	Sequence 10, Appl
c 24	30.2	15.9	536	6	US-09-925-065A-775979	Sequence 775979,
c 25	30	15.8	527	6	US-09-925-065A-470490	Sequence 470490,
c 26	30	15.8	616	10	US-10-301-480-576573	Sequence 576573,
c 27	30	15.8	616	10	US-10-301-480-1189982	Sequence 1189982,
c 28	30	15.8	1548	8	US-10-750-185-48300	Sequence 48300, A
c 29	30	15.8	1548	8	US-10-750-623-48300	Sequence 48300, A
c 30	30	15.8	1797	6	US-09-925-065A-701082	Sequence 701082,
c 31	29.4	15.5	694	6	US-09-925-065A-86731	Sequence 86731, A
c 32	29.4	15.5	694	6	US-09-925-065A-86732	Sequence 86732, A
c 33	29.4	15.5	694	9	US-10-301-480-187971	Sequence 187971,
c 34	29.4	15.5	694	9	US-10-301-480-187972	Sequence 187972,
c 35	29.4	15.5	694	10	US-10-301-480-801380	Sequence 801380,
c 36	29.4	15.5	694	10	US-10-301-480-801381	Sequence 801381,
c 37	29.4	15.5	25988	9	US-10-330-773-219	Sequence 219, App
c 38	29	15.3	613	6	US-09-925-065A-692964	Sequence 692964,
c 39	28.8	15.2	641	6	US-09-925-065A-88244	Sequence 88244, A
c 40	28.8	15.2	641	9	US-10-301-480-189485	Sequence 189485,
c 41	28.8	15.2	641	10	US-10-301-480-802894	Sequence 802894,
c 42	28.8	15.2	110608	8	US-10-775-189-193	Sequence 193, App
c 43	28.4	14.9	481	6	US-09-925-065A-317205	Sequence 317205,
c 44	28.4	14.9	484	10	US-10-301-480-392136	Sequence 392136,
c 45	28.4	14.9	484	10	US-10-301-480-1005545	Sequence 1005545,

ALIGNMENTS

RESULT 1

US-11-005-216-3
; Sequence 3, Application US/11005216
; Publication No. US20050287633A1
; GENERAL INFORMATION:
; APPLICANT: Mcintyre, Peter
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/11/005,216
; PRIOR FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US/09/533,220
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30
; SEQ ID NO 3
; LENGTH: 5155
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-005-216-3

Query Match	26.0%	Score 49.4;	DB 14;	Length 5155;
Best Local Similarity	83.6%	Pred. No. 2.7e-05;		
Matches	56;	Conservative	0;	Mismatches 11; Indels 0; Gaps 0;
Qy	82	CCGGTGTTCCTGAAGGGCGCTATATAGGGGGGGCGGCGGTCGTCCTCATCTCGA	141	
Db	567	CGGGTGTTCCTGAAGGGGGCTATAAAGGGGGTGGGGCGGTCGTCCTCATCTCTT	626	
Qy	142	CCGGCTC	148	
Db	627	CCGCATC	633	

RESULT 2

US-11-077-716-1
; Sequence 1, Application US/1107716
; Publication No. US20050260180A1
; GENERAL INFORMATION:

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:20:15 ; Search time 247.814 Seconds
(without alignments)
6340.158 Million cell updates/sec

Title: US-10-781-055A-35

Perfect score: 190

Sequence: 1 aaatgacataggaaactga.....ctctcagtcctcagcgatcaa 190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	190	7	US-10-781-055-35
2	190	100.0	596	7	US-10-781-055-37
3	190	100.0	614	7	US-10-781-055-36
4	49.4	26.0	3788	3	US-09-392-462-1
5	49.4	26.0	3788	3	US-09-540-991-1
6	49.4	26.0	3788	6	US-10-291-041-1
7	49.4	26.0	3788	7	US-10-351-603-1
8	49.4	26.0	5155	5	US-10-128-853-3
9	49.4	26.0	5374	5	US-10-007-357-7
10	49.4	26.0	5462	5	US-10-007-357-6
11	49.4	26.0	7522	8	US-10-491-121-36
12	49.4	26.0	7711	7	US-10-359-120-49
13	49.4	26.0	7711	8	US-10-491-121-35
14	49.4	26.0	7789	7	US-10-359-120-45
15	49.4	26.0	7789	7	US-10-359-120-48
16	49.4	26.0	7792	7	US-10-359-120-46
17	49.4	26.0	7828	7	US-10-359-120-47
18	49.4	26.0	7867	7	US-10-359-120-42
19	49.4	26.0	7870	7	US-10-359-120-39
20	49.4	26.0	7870	7	US-10-359-120-43
21	49.4	26.0	7885	7	US-10-359-120-44
22	49.4	26.0	7906	7	US-10-359-120-40
23	49.4	26.0	7909	7	US-10-359-120-41

Sequence 36, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 35, Appl
Sequence 12, Appl
Sequence 20, Appl
Sequence 29, Appl
Sequence 27, Appl
Sequence 50, Appl
Sequence 32, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 25, Appl
Sequence 4, Appl
Sequence 19, Appl
Sequence 49, Appl
Sequence 3, Appl
Sequence 507, App
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-10-781-055-35
; Sequence 35, Application US/10781055
; Publication No. US20040171573A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN
; APPLICANT: QU, BAO-XI
; TITLE OF INVENTION: RATIONALLY DESIGNED AND CHEMICALLY SYNTHESIZED
; FILE REFERENCE: PROMOTER FOR GENETIC VACCINE AND GENE THERAPY
; FILE REFERENCE: UTSD:788US
; CURRENT APPLICATION NUMBER: US/10/781,055
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/448,166
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-781-055-35

Query Match 100.0%; Score 190; DB 7; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAATGACATAGGAAACTGACTCAAAAGGAGAGTGAAGTGGGACTTTCCAAAGGCG	60
Db	1	AAATGACATAGGAAACTGACTCAAAAGGAGAGTGAAGTGGGACTTTCCAAAGGCG	60
Qy	61	GGCCAAATTGGGGGGGGCCACCGGTCTCTCTGAAGGCGGCTATATAAGGGGGGGCGGG	120
Db	61	GGCCAAATTGGGGGGGGCCACCGGTCTCTCTGAAGGCGGCTATATAAGGGGGGGCGGG	120
Qy	121	CGCGTTCTGCTCTCATTTCTGGACCGCGTCCGCGCCCGGAGCAGCTGAGCTCTCAGTCT	180
Db	121	CGCGTTCTGCTCTCATTTCTGGACCGCGTCCGCGCCCGGAGCAGCTGAGCTCTCAGTCT	180
Qy	181	CAGCGATCAA 190	
Db	181	CAGCGATCAA 190	

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:03:35 ; Search time 50.7571 Seconds
(without alignments)
6653.974 Million cell updates/sec

Title: US-10-781-055A-35
Perfect score: 190
Sequence: 1 aaatgaataggaaactga.....ctctcagtcctcagcgatcaa 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgm2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgm2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgm2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/1/ina/H COMB.seq.*
6: /cgm2_6/ptodata/1/ina/PCBUS COMB.seq.*
7: /cgm2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgm2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	26.0	382	2	US-08-333-706-1
2	49.4	26.0	643	2	US-08-458-372-21
3	49.4	26.0	643	8	US-09-384-327-21
4	49.4	26.0	872	2	US-08-458-372-20
5	49.4	26.0	872	8	US-09-384-327-20
6	49.4	26.0	874	9	US-06118-10
7	49.4	26.0	2898	9	US-09-051-696-7
8	49.4	26.0	5155	3	US-09-533-220A-3
9	49.4	26.0	5155	3	US-10-128-853-3
10	49.4	26.0	5374	3	US-10-007-357-7
11	49.4	26.0	5462	3	US-10-007-357-6
12	49.4	26.0	6151	6	PCT-US91-02954-12
13	49.4	26.0	6306	6	PCT-US94-00658-1
14	49.4	26.0	32166	3	US-09-562-930-11
15	49.4	26.0	32798	3	US-09-604-694B-1
16	49.4	26.0	34303	2	US-08-735-609-4
17	49.4	26.0	34303	2	US-08-735-609-4
18	49.4	26.0	34303	3	US-09-315-372-4
19	49.4	26.0	34303	3	US-09-244-752-4
20	49.4	26.0	34303	3	US-09-245-497-4
21	49.4	26.0	34303	3	US-09-562-919-4
22	49.4	26.0	34382	2	US-08-374-483-6
23	49.4	26.0	34427	3	US-09-111-911-5
24	49.4	26.0	35408	3	US-08-973-334-3

25	49.4	26.0	35408	3	US-09-563-869A-3	Sequence 3, Appli
26	49.4	26.0	35408	3	US-08-549-489-3	Sequence 3, Appli
27	49.4	26.0	35871	3	US-09-956-335-2	Sequence 2, Appli
28	49.4	26.0	35935	2	US-08-735-609-1	Sequence 1, Appli
29	49.4	26.0	35935	2	US-08-735-609-1	Sequence 1, Appli
30	49.4	26.0	35935	3	US-08-379-452-43	Sequence 43, Appl
31	49.4	26.0	35935	3	US-09-315-372-1	Sequence 1, Appli
32	49.4	26.0	35935	3	US-09-244-752-1	Sequence 1, Appli
33	49.4	26.0	35935	3	US-09-245-497-1	Sequence 1, Appli
34	49.4	26.0	35935	3	US-09-409-670-43	Sequence 43, Appl
35	49.4	26.0	35935	3	US-09-562-919-1	Sequence 1, Appli
36	49.4	26.0	35935	3	US-09-782-378A-4	Sequence 4, Appli
37	49.4	26.0	35935	3	US-09-782-378A-5	Sequence 5, Appli
38	49.4	26.0	35937	3	US-09-782-378A-3	Sequence 3, Appli
39	49.4	26.0	35978	3	US-09-956-335-1	Sequence 1, Appli
40	49.4	26.0	36620	3	US-09-952-060-30	Sequence 30, Appl
41	49.4	26.0	37474	3	US-09-952-060-25	Sequence 25, Appl
42	49.4	26.0	38519	3	US-09-952-060-28	Sequence 28, Appl
43	47.8	25.2	12445	3	US-09-865-022-2	Sequence 2, Appli
44	42	22.1	50	2	US-08-171-389-579	Sequence 579, App
45	42	22.1	50	2	US-08-171-389-580	Sequence 580, App

ALIGNMENTS

RESULT 1
US-08-333-706-1
; Sequence 1, Application US/08333706
; Patent No. 5612213
; GENERAL INFORMATION:
; APPLICANT: Chan, Shan-Yuen
; TITLE OF INVENTION: Vector and Mammalian Cell Line Having Improved
; TITLE OF INVENTION: Productivity
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: Fourth and Parker Streets
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/075,209
; FILING DATE: 10-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: CL-208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)420-5511
; TELEFAX: (510)428-4703
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-333-706-1

Query Match 26.0%; Score 49.4; DB 2; Length 382;
Best Local Similarity 83.6%; Pred. No. 1.5e-06;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:52:47 ; Search time 1231.06 Seconds
(without alignments)
7221.025 Million cell updates/sec

Title: US-10-781-055A-35

Perfect score: 190

Sequence: 1 aaatgacataggaactga.....ctctcagtcacgcatcaa 190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_est8.*

9: gb_gss1.*

10: gb_gss2.*

11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	19.5	1068	3	BM921844
2	36.8	19.4	984	10	CZ386907 ZMMBF0163
3	36.4	19.2	549	10	CZ439879 OA_BBa009
4	35.6	18.7	846	8	DR408103
5	35.4	18.6	918	10	AG841160 Oryza sat
6	34.8	18.3	608	8	DN871503 nad13h05.
7	34.6	18.2	674	10	CE814538 tigr-gss-
8	34.4	18.1	754	9	AQ288311 abxb0032L
9	34.4	18.1	1078	8	DR147979 49078488
10	34.2	18.0	758	2	BG395886 602458681
11	34.2	18.0	2225	4	BC033179 Homo sapi
12	34	17.9	636	10	CL770232
13	34	17.9	717	9	AQ419418 RPT-11-2
14	34	17.9	1302	3	BM456102
15	34	17.9	1494	3	BQ059578
16	33.8	17.8	1149	10	CL972671
17	33.6	17.7	333	5	BY150204
18	33.6	17.7	610	3	BI393079
19	33.6	17.7	643	3	BI390903
20	33.6	17.7	705	10	CZ426480
21	33.6	17.7	708	10	CZ406542
22	33.6	17.7	822	5	BU159228

C	23	33.6	17.7	827	10	CZ353914	CZ353914 ZMMBF0091
	24	33.6	17.7	943	10	CZ399845	CZ399845 ZMMBF0181
	25	33.6	17.7	1113	3	BI872862	BI872862 603397470
	26	33.4	17.6	374	2	BE955554	BE955554 UI-M-CE1-
	27	33.4	17.6	779	3	BI601205	BI601205 603245717
	28	33.4	17.6	1112	8	DR737645	DR737645 EGSAS08286
	29	33.2	17.5	289	2	BB870121	BB870121 BB870121
	30	33.2	17.5	606	8	DN436751	DN436751 LIB4217-0
	31	33.2	17.5	673	8	DN416974	DN416974 LIB4215-0
	32	33.2	17.5	1045	10	CL495014	CL495014 SAIL_604
	33	33	17.4	334	5	BY794202	BY794202 BY794202
	34	33	17.4	390	10	CE848591	CE848591 tigr-gss-
	35	33	17.4	458	7	CF853400	CF853400 psmC008xk
	36	33	17.4	615	3	BI382039	BI382039 BFLG2_000
	37	33	17.4	694	7	CK807009	CK807009 AGENCOURT
	38	33	17.4	1152	10	AG048286	AG048286 Pan trogl
	39	33	17.4	1378	3	BM807238	BM807238 AGENCOURT
	40	33	17.4	1664	10	AG082918	AG082918 Pan trogl
	41	32.8	17.3	490	8	CX802784	CX802784 JGI_CAAJ1
	42	32.8	17.3	582	3	BP303844	BP303844 BP303844
	43	32.8	17.3	621	2	BF673001	BF673001 602152887
	44	32.8	17.3	747	6	CA170582	CA170582 SCQSS9105
	45	32.8	17.3	948	2	BG397609	BG397609 602438652

ALIGNMENTS

RESULT 1
BM921844
LOCUS
DEFINITION
5', mRNA sequence.
AGENCOURT_6706906 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753443
1068 bp mRNA linear EST 12-MAR-2002
BM921844
ACCESSION
BM921844
VERSION
BM921844.1 GI:19372223
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 1068)
NIH-MGC <http://mgc.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLAM12789 row: d column: 20
High quality sequence stop: 270.
Location/Qualifiers
1..1068
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5753443"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code

FEATURES
source

GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:41:05 ; Search time 172.221 Seconds
(without alignments)
7352.695 Million cell updates/sec

Title: US-10-781-055A-35

Perfect score: 190

Sequence: 1 aaatgacataggaaactga.....ctctcagtcctcagcgatcaaa 190

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	100.0	190	13 ADR90242	ADR90242 SP72 prom
2	190	100.0	596	13 ADR90244	ADR90244 SP72 prom
3	190	100.0	614	13 ADR90243	ADR90243 SP72 prom
4	49.4	26.0	382	2 AAT79748	AAT79748 AML promo
5	49.4	26.0	382	2 AAT60502	AAT60502 Adeno maj
6	49.4	26.0	382	2 AAT62387	AAT62387 Nucleotid
7	49.4	26.0	561	1 AAN50287	AAN50287 Sequence
8	49.4	26.0	578	1 AAN50288	AAN50288 Sequence
9	49.4	26.0	642	2 AAQ54210	AAQ54210 BK enhanc
10	49.4	26.0	642	2 AAQ58456	AAQ58456 BK enhanc
11	49.4	26.0	642	2 AAT15956	AAT15956 BK enhanc
12	49.4	26.0	642	2 AAT95172	AAT95172 Sequence
13	49.4	26.0	824	1 AAN70083	AAN70083 Sequence
14	49.4	26.0	848	2 AAQ13632	AAQ13632 GBMT modi
15	49.4	26.0	873	3 AAQ39104	AAQ39104 Plasmid p
16	49.4	26.0	874	1 AAN70082	AAN70082 Sequence
17	49.4	26.0	874	2 AAQ03825	AAQ03825 Improved
18	49.4	26.0	874	2 AAQ54209	AAQ54209 BK enhanc
19	49.4	26.0	874	2 AAQ58455	AAQ58455 BK enhanc

20	49.4	26.0	874	2 AAT36645	AAT36645 BK enhanc
21	49.4	26.0	874	2 AAT15955	AAT15955 BK enhanc
22	49.4	26.0	874	2 AAT43793	AAT43793 BK enhanc
23	49.4	26.0	874	2 AAT95171	AAT95171 BK enhanc
24	49.4	26.0	874	2 AAX18483	AAX18483 BK enhanc
25	49.4	26.0	874	5 AAX45120	AAX45120 BK protot
26	49.4	26.0	3788	3 AAT293330	AAT293330 PGZA-CAT
27	49.4	26.0	3788	5 AAD21318	AAD21318 CpG alter
28	49.4	26.0	5155	6 AAD42468	AAD42468 Human pla
29	49.4	26.0	5155	8 ACA61961	ACA61961 Mammalian
30	49.4	26.0	5365	1 AAN90646	AAN90646 Nucleotid
31	49.4	26.0	5374	3 AAC60706	AAC60706 Primers a
32	49.4	26.0	5413	1 AAN90649	AAN90649 Nucleotid
33	49.4	26.0	5462	3 AAC60707	AAC60707 Primers a
34	49.4	26.0	5518	1 AAN90647	AAN90647 Nucleotid
35	49.4	26.0	5566	1 AAN90648	AAN90648 Nucleotid
36	49.4	26.0	6149	1 AAN90645	AAN90645 Sequence
37	49.4	26.0	6151	1 AAN90644	AAN90644 Sequence
38	49.4	26.0	6151	2 AAQ05608	AAQ05608 Plasmid p
39	49.4	26.0	6151	2 AAQ03006	AAQ03006 Full leng
40	49.4	26.0	6165	2 AAQ20324	AAQ20324 Sol.rhesu
41	49.4	26.0	7316	2 AAQ04555	AAQ04555 Plasmid p
42	49.4	26.0	7377	2 AAQ05607	AAQ05607 Plasmid p
43	49.4	26.0	7377	2 AAQ03005	AAQ03005 Full leng
44	49.4	26.0	7522	10 ACC71556	ACC71556 VRC6811 (
45	49.4	26.0	7711	6 ABK91497	ABK91497 Modified

ALIGNMENTS

RESULT 1

ADR90242

ID ADR90242 standard; DNA; 190 BP.

AC ADR90242;

DT 18-NOV-2004 (first entry)

XX SP72 promoter DNA #1.

DE Promoter/enhancer; cancer; infectious disease; inflammatory disease;

KW tuberculosis; hepatitis B; HIV-1; influenza; malaria; cytostatic;

KW vaccine; gene therapy; SP72 promoter; ds.

XX Unidentified.

XX US2004171573-A1.

PN 02-SEP-2004.

XX 18-FEB-2004; 2004US-00781055.

XX 18-FEB-2003; 2003US-0448166P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Johnston S, Qu B;

XX WPI; 2004-634560/61.

XX New nucleic acid segment comprises SP72 synthetic promoter/enhancer, useful as a vaccine for genetic immunization or for gene therapy for treating or preventing cancers, infectious diseases, or inflammatory diseases.

XX Claim 12; SEQ ID NO 35; 34pp; English.

XX The present invention provides nucleic acid segments comprising a synthetic promoter/enhancer or its complement. The invention is useful for treating or preventing diseases or conditions including cancers, infectious diseases and inflammatory diseases such as viral and parasitic including tuberculosis, hepatitis B, HIV-1, influenza and malaria. The

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 28, 2006, 05:46:12 ; Search time 1034.96 Seconds
(without alignments)
10435.462 Million cell updates/sec

Title: US-10-781-055A-35
Perfect score: 190
Sequence: 1 aaatgacataggaactga.....ctctcagctcagcgatcaa 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5883141 seqs, 28421725653 residues 11766282
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	26.0	382	6	I36987 Sequence 1
2	49.4	26.0	560	6	I02395 Sequence 1
3	49.4	26.0	578	6	I02396 Sequence 2
4	49.4	26.0	642	6	E01427 DNA sequenc
5	49.4	26.0	642	6	E59622 Human prote
6	49.4	26.0	642	6	I05120 Sequence 11
7	49.4	26.0	642	6	BD014699 Recombina
8	49.4	26.0	643	6	I71451 Sequence 21
9	49.4	26.0	872	6	I71450 Sequence 20
10	49.4	26.0	874	6	E01426 DNA sequenc
11	49.4	26.0	874	6	E59621 Human prote
12	49.4	26.0	874	6	I05111 Sequence 10
13	49.4	26.0	874	6	I07642 Sequence 11
14	49.4	26.0	874	6	AR365523 Sequence
15	49.4	26.0	874	6	BD014698 Recombina
16	49.4	26.0	2898	6	ARI78237 Sequence
17	49.4	26.0	3788	6	BD223711 Methylati
18	49.4	26.0	3788	6	AX282868 Sequence

19	49.4	26.0	5155	6	AR214348 Sequence
20	49.4	26.0	5155	6	AR654117 Sequence
21	49.4	26.0	5365	6	I09267 Sequence 34
22	49.4	26.0	5374	6	BD247396 Primer-as
23	49.4	26.0	5374	6	AR533276 Sequence
24	49.4	26.0	5413	6	I09270 Sequence 37
25	49.4	26.0	5462	6	BD247395 Primer-as
26	49.4	26.0	5462	6	AR533275 Sequence
27	49.4	26.0	5518	6	I09268 Sequence 35
28	49.4	26.0	5566	6	I09269 Sequence 36
29	49.4	26.0	6149	6	I09252 Sequence 19
30	49.4	26.0	6151	6	I09251 Sequence 18
31	49.4	26.0	7069	11	U02442 Cloning vec
32	49.4	26.0	7711	6	AX427811 Sequence
33	49.4	26.0	7789	6	AX427807 Sequence
34	49.4	26.0	7789	6	AX427810 Sequence
35	49.4	26.0	7792	6	AX427808 Sequence
36	49.4	26.0	7819	6	CS078969 Sequence
37	49.4	26.0	7828	6	AX427809 Sequence
38	49.4	26.0	7841	6	CS078964 Sequence
39	49.4	26.0	7844	6	CS078966 Sequence
40	49.4	26.0	7852	6	CS078967 Sequence
41	49.4	26.0	7867	6	AX427804 Sequence
42	49.4	26.0	7870	6	AX427801 Sequence
43	49.4	26.0	7870	6	AX427805 Sequence
44	49.4	26.0	7885	6	AX427806 Sequence
45	49.4	26.0	7906	6	AX427802 Sequence

ALIGNMENTS

RESULT 1
I36987
LOCUS Sequence 1 382 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5612213.
ACCESSION I36987
VERSION I36987.1 GI:2084947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 382)
AUTHORS Chan, S. Y.
TITLE Method of selecting mammalian cell lines having improved productivity
JOURNAL Patent: US 5612213-A 1 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..382
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 26.0%; Score 49.4; DB 6; Length 382;
Best Local Similarity 83.6%; Pred. No. 0.013;
Matches 56; Conservative 11; Indels 0; Gaps 0;
QY 82 CCGGTGTTCTTGAAGGGCGCCCTATATAAGGGGGGGCGGCGTTCGTCCTCATCTGGA 141
Db 197 CGGGTCTTCTGAAGGGGGCGCTATAAAGGGGGTGGGGCGGCGTTCGTCCTCATCTCTT 256
QY 142 CCGCGTC 148
Db 257 CCGCATC 263

RESULT 2
I02395
LOCUS Sequence 1 560 bp ss-DNA linear PAT 18-MAY-1993
DEFINITION Sequence 1 from Patent US 4510245.
ACCESSION I02395
VERSION I02395.1 GI:268039
KEYWORDS

Result No.	Score	Query Match	SAMPLES			Description
			Length	ID	DB	
1	49.4	8.3	5155	14	US-11-005-216-3	Sequence 3, Appli
2	49.4	8.3	33014	14	US-11-077-716-1	Sequence 1, Appli
3	49.4	8.3	33592	11	US-11-249-873-1	Sequence 1, Appli
4	49.4	8.3	33699	11	US-11-249-873-3	Sequence 3, Appli
5	49.4	8.3	33988	11	US-11-249-873-14	Sequence 14, Appli
6	49.4	8.3	34341	11	US-11-249-873-2	Sequence 2, Appli
7	49.4	8.3	34448	11	US-11-249-873-4	Sequence 4, Appli
8	49.4	8.3	34555	8	US-10-623-155-479	Sequence 479, App
9	49.4	8.3	34737	11	US-11-249-873-15	Sequence 15, App
10	49.4	8.3	35696	8	US-10-860-436-1	Sequence 1, Appli
11	49.4	8.3	35724	11	US-11-249-873-13	Sequence 13, Appli
12	49.4	8.3	35893	8	US-10-860-436-2	Sequence 2, Appli
13	49.4	8.3	35935	14	US-11-127-832-4	Sequence 4, Appli
14	49.4	8.3	35935	14	US-11-127-832-5	Sequence 5, Appli
15	49.4	8.3	35937	14	US-11-127-832-3	Sequence 3, Appli
16	49.4	8.3	36114	11	US-11-249-873-16	Sequence 16, Appli
17	47.8	8.0	12445	9	US-10-948-344-2	Sequence 2, Appli
18	37.4	6.3	1815	9	US-10-933-182A-76020	Sequence 76020, A

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:03:35 ; Search time 159.217 Seconds
(without alignments)
6653.974 Million cell updates/sec

Title: US-10-781-055A-37

Perfect score: 596

Sequence: 1 cgggtacagatgttcgat.....ctctcagtcagcagatcaa 596

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	8.3	382	2	US-08-333-706-1
2	49.4	8.3	643	2	US-08-458-372-21
3	49.4	8.3	643	8	US-09-384-327-21
4	49.4	8.3	872	2	US-08-458-372-20
5	49.4	8.3	872	8	US-09-384-327-20
6	49.4	8.3	874	9	5506118-10
7	49.4	8.3	2898	3	US-09-051-696-7
8	49.4	8.3	5155	3	US-09-533-220A-3
9	49.4	8.3	5374	3	US-10-128-853-3
10	49.4	8.3	5374	3	US-10-007-357-7
11	49.4	8.3	5462	3	US-10-007-357-6
12	49.4	8.3	6151	6	PCT-US91-02954-12
13	49.4	8.3	6306	6	PCT-US94-00658-1
14	49.4	8.3	32166	3	US-09-562-930-11
15	49.4	8.3	32798	3	US-09-604-6948-1
16	49.4	8.3	34303	2	US-08-735-609-4
17	49.4	8.3	34303	2	US-08-735-609-4
18	49.4	8.3	34303	3	US-09-315-372-4
19	49.4	8.3	34303	3	US-09-244-752-4
20	49.4	8.3	34303	3	US-09-245-497-4
21	49.4	8.3	34303	3	US-09-562-919-4
22	49.4	8.3	34382	2	US-08-374-483-6
23	49.4	8.3	34427	3	US-09-111-911-5
24	49.4	8.3	35408	3	US-08-973-334-3

25	49.4	8.3	35408	3	US-09-563-869A-3	Sequence 3, Appli	
26	49.4	8.3	35408	3	US-08-549-489-3	Sequence 3, Appli	
27	49.4	8.3	35871	3	US-09-956-335-2	Sequence 2, Appli	
28	49.4	8.3	35935	2	US-08-735-609-1	Sequence 1, Appli	
29	49.4	8.3	35935	2	US-08-735-609-1	Sequence 1, Appli	
30	49.4	8.3	35935	3	US-08-379-452-43	Sequence 43, Appli	
31	49.4	8.3	35935	3	US-09-315-372-1	Sequence 1, Appli	
32	49.4	8.3	35935	3	US-09-244-752-1	Sequence 1, Appli	
33	49.4	8.3	35935	3	US-09-245-497-1	Sequence 1, Appli	
34	49.4	8.3	35935	3	US-09-409-670-43	Sequence 43, Appli	
35	49.4	8.3	35935	3	US-09-562-919-1	Sequence 1, Appli	
36	49.4	8.3	35935	3	US-09-782-378A-4	Sequence 4, Appli	
37	49.4	8.3	35935	3	US-09-782-378A-5	Sequence 5, Appli	
38	49.4	8.3	35937	3	US-09-782-378A-3	Sequence 3, Appli	
39	49.4	8.3	35978	3	US-09-956-335-1	Sequence 1, Appli	
40	49.4	8.3	36620	3	US-09-952-060-30	Sequence 30, Appli	
41	49.4	8.3	37474	3	US-09-952-060-25	Sequence 25, Appli	
42	49.4	8.3	38519	3	US-09-952-060-28	Sequence 28, Appli	
43	47.8	8.0	12445	3	US-09-865-032-2	Sequence 2, Appli	
c	44	44.8	7.5	7218	2	US-08-232-463-14	Sequence 14, Appli
45	42	7.0	50	2	US-08-171-389-579	Sequence 579, Appli	

ALIGNMENTS

RESULT 1

US-08-333-706-1
; Sequence 1, Application US/08333706
; Patent No. 5612213
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; TITLE OF INVENTION: Vector and Mammalian Cell Line Having Improved
; TITLE OF INVENTION: Productivity
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: Fourth and Parker Streets
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,706
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/075,209
; FILING DATE: 10-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: CL-208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)420-5511
; TELEFAX: (510)428-4703
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-333-706-1

Query Match 8.3%; Score 49.4; DB 2; Length 382;
Best Local Similarity 83.6%; Fred. No. 9.6e-06;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:52:47 ; Search time 3861.65 Seconds
(without alignments)
7221.025 Million cell updates/sec

Title: US-10-781-055A-37

Perfect score: 596

Sequence: 1 cggtagatgatgtcttcgat.....ctctcagtcctcagcgatcaa 596

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs; 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	47.6	8.0	1151	10	CL048546 CH216-68C
C 2	39.6	6.6	1201	10	AL106532 Drosophila
C 3	38.8	6.5	859	10	AL055406 Drosophila
C 4	38.2	6.4	1068	3	BM921844 AGENCOURT
C 5	38	6.4	409	1	AI857142 MENAd-A1
C 6	37.4	6.3	796	7	CR412210 CH21210
C 7	37.2	6.2	1079	9	CC230752 CH261-114
C 8	36.8	6.2	568	6	CD125835 MF1-0001U
C 9	36.8	6.2	584	10	CZ386907 ZMMBF0163
C 10	36.8	6.2	997	10	CNS005TE
C 11	36.6	6.1	794	8	DN112025 1111185 M
C 12	36.4	6.1	549	10	C2439879
C 13	36.4	6.1	821	5	BX731308 BX731308
C 14	36.4	6.1	1064	9	BZ247726 CH230-457
C 15	36.4	6.1	1200	6	CD503874
C 16	36.2	6.1	655	10	CE451080 tigr-gss-
C 17	36.2	6.1	914	1	AL544144 AL544144
C 18	36	6.0	612	9	BH679464 BOHW233TF
C 19	36	6.0	737	8	DR399051
C 20	36	6.0	1030	10	CNS02082
C 21	35.6	6.0	589	10	CE343398 tigr-gss-
C 22	35.6	6.0	846	8	DR408103 mhn20d02.

23	35.6	6.0	1078	6	CF223929
24	35.4	5.9	360	5	C61810
C 25	35.4	5.9	444	9	AQ767046
26	35.4	5.9	737	10	AG436603
C 27	35.4	5.9	817	10	CZ998292
C 28	35.4	5.9	856	11	CNS035DM
C 29	35.4	5.9	918	10	AG841160
C 30	35.4	5.9	1113	8	DN667583
31	35.4	5.9	1201	5	EX377655
32	35.2	5.9	677	9	BZ412845
C 33	35.2	5.9	747	7	CO393315
C 34	35.2	5.9	831	6	CB558496
C 35	35	5.9	451	3	BJ898349
C 36	35	5.9	710	2	BE034031
37	35	5.9	840	9	AZ212232
38	35	5.9	884	10	CZ209683
C 39	35	5.9	1014	10	CL109372
40	35	5.9	1112	8	DR737645
41	34.8	5.8	227	8	M79041
42	34.8	5.8	339	8	M79042
43	34.8	5.8	415	9	AQ755672
C 44	34.8	5.8	608	8	DN871503
45	34.8	5.8	698	8	CV850179

ALIGNMENTS

RESULT 1
CL048546/c
LOCUS
DEFINITION
CH216-68C22_RM1.1 CH216 Xenopus tropicalis genomic clone
CH216-68C22, genomic survey sequence.
CL048546
GSS.
CL048546.1 GI:40504459
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 1151)
Kreititzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
CONTACT: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGAGA
Class: BAC ends
High quality sequence start: 25
High quality sequence stop: 438.
FEATURES
source
1..1151
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-68C22"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN

Query Match 8.0%; Score 47.6; DB 10; Length 1151;
Best Local Similarity 50.9%; Pred No. 0.0068;
Matches 113; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:41:05 ; Search time 540.231 Seconds
(without alignments)
7352.695 Million cell updates/sec

Title: US-10-781-055A-37
Perfect score: 596
Sequence: 1 cggatcatgtgtctcgat.....ctctcagtcacgcatcaa 596

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	596	13	ADR90244
2	568	95.3	614	13	ADR90243
3	190	31.9	190	13	ADR90242
4	60	10.1	60	13	ADR90218
5	51	8.6	51	13	ADR90216
6	49.4	8.3	382	2	AAQ79748
7	49.4	8.3	382	2	AAQ79748
8	49.4	8.3	382	2	AAQ79748
9	49.4	8.3	382	2	AAQ79748
10	49.4	8.3	382	2	AAQ79748
11	49.4	8.3	382	2	AAQ79748
12	49.4	8.3	382	2	AAQ79748
13	49.4	8.3	382	2	AAQ79748
14	49.4	8.3	382	2	AAQ79748
15	49.4	8.3	382	2	AAQ79748
16	49.4	8.3	382	2	AAQ79748
17	49.4	8.3	382	2	AAQ79748
18	49.4	8.3	382	2	AAQ79748
19	49.4	8.3	382	2	AAQ79748

20	49.4	8.3	874	2	AAQ54209
21	49.4	8.3	874	2	AAQ58455
22	49.4	8.3	874	2	AAQ58455
23	49.4	8.3	874	2	AAQ58455
24	49.4	8.3	874	2	AAQ58455
25	49.4	8.3	874	2	AAQ58455
26	49.4	8.3	874	2	AAQ58455
27	49.4	8.3	874	2	AAQ58455
28	49.4	8.3	874	2	AAQ58455
29	49.4	8.3	874	2	AAQ58455
30	49.4	8.3	874	2	AAQ58455
31	49.4	8.3	874	2	AAQ58455
32	49.4	8.3	874	2	AAQ58455
33	49.4	8.3	874	2	AAQ58455
34	49.4	8.3	874	2	AAQ58455
35	49.4	8.3	874	2	AAQ58455
36	49.4	8.3	874	2	AAQ58455
37	49.4	8.3	874	2	AAQ58455
38	49.4	8.3	874	2	AAQ58455
39	49.4	8.3	874	2	AAQ58455
40	49.4	8.3	874	2	AAQ58455
41	49.4	8.3	874	2	AAQ58455
42	49.4	8.3	874	2	AAQ58455
43	49.4	8.3	874	2	AAQ58455
44	49.4	8.3	874	2	AAQ58455
45	49.4	8.3	874	2	AAQ58455

ALIGNMENTS

RESULT 1

ADR90244
ID ADR90244 standard; DNA; 596 BP.

AC ADR90244;

DT 18-NOV-2004 (first entry)

DE SP72 promoter DNA #3.

XX Promoter/enhancer; cancer; infectious disease; inflammatory disease;

KW tuberculosis; hepatitis B; HIV-1; influenza; malaria; cytostatic;

KW vaccine; gene therapy; SP72 promoter; ds.

XX Unidentified.

OS Unidentified.

XX US2004171573-A1.

XX 02-SEP-2004.

XX 18-FEB-2004; 2004US-00781055.

XX 18-FEB-2003; 2003US-0448166P.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Johnston S, Qu B;

XX WPI; 2004-634560/61.

DR New nucleic acid segment comprises SP72 synthetic promoter/enhancer,

PT useful as a vaccine for genetic immunization or for gene therapy for

PT treating or preventing cancers, infectious diseases, or inflammatory

PT diseases.

PS Claim 14; SEQ ID NO 37; 34pp; English.

XX The present invention provides nucleic acid segments comprising a

CC synthetic promoter/enhancer or its complement. The invention is useful

CC for treating or preventing diseases or conditions including cancers,

CC infectious diseases and inflammatory diseases such as viral and parasitic

CC including tuberculosis, hepatitis B, HIV-1, influenza and malaria. The

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:46:12 ; Search time 3246.5 Seconds
(without alignments)
10435.462 Million cell updates/sec

Title: US-10-781-055A-37

Perfect score: 596

Sequence: 1 cggatcatgatgttctcgat.....ctctcagtcgcgatcaa 596

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sta.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49.4	8.3	382	6 I36987	I36987 Sequence 1
2	49.4	8.3	560	6 I02395	I02395 Sequence 1
3	49.4	8.3	578	6 I02396	I02396 Sequence 2
4	49.4	8.3	642	6 E01427	E01427 DNA sequenc
5	49.4	8.3	642	6 E59622	E59622 Human prote
6	49.4	8.3	642	6 I05120	I05120 Sequence 11
7	49.4	8.3	642	6 BD014699	BD014699 Recombina
8	49.4	8.3	643	6 I71451	I71451 Sequence 21
9	49.4	8.3	872	6 I71450	I71450 Sequence 20
10	49.4	8.3	874	6 E01426	E01426 DNA sequenc
11	49.4	8.3	874	6 E59621	E59621 Human prote
12	49.4	8.3	874	6 I05111	I05111 Sequence 10
13	49.4	8.3	874	6 I07642	I07642 Sequence 11
14	49.4	8.3	874	6 AR365523	AR365523 Sequence
15	49.4	8.3	874	6 BD014698	BD014698 Recombina
16	49.4	8.3	2898	6 ARL78237	ARL78237 Sequence
17	49.4	8.3	3788	6 BD223711	BD223711 Methylati
18	49.4	8.3	3788	6 AX282868	AX282868 Sequence

19	49.4	8.3	5155	6 AR214348	AR214348 Sequence
20	49.4	8.3	5155	6 AR654117	AR654117 Sequence
21	49.4	8.3	5365	6 I09267	I09267 Sequence 34
22	49.4	8.3	5374	6 BD247396	BD247396 Primer-as
23	49.4	8.3	5374	6 AR533276	AR533276 Sequence 37
24	49.4	8.3	5413	6 I09270	I09270 Sequence 37
25	49.4	8.3	5462	6 BD247395	BD247395 Primer-as
26	49.4	8.3	5462	6 AR533275	AR533275 Sequence 35
27	49.4	8.3	5518	6 I09268	I09268 Sequence 35
28	49.4	8.3	5566	6 I09269	I09269 Sequence 36
29	49.4	8.3	6149	6 I09252	I09252 Sequence 19
30	49.4	8.3	6151	6 I09251	I09251 Sequence 18
31	49.4	8.3	7069	11 U02442	U02442 cloning vec
32	49.4	8.3	7711	6 AX427811	AX427811 Sequence
33	49.4	8.3	7789	6 AX427807	AX427807 Sequence
34	49.4	8.3	7789	6 AX427810	AX427810 Sequence
35	49.4	8.3	7792	6 AX427808	AX427808 Sequence
36	49.4	8.3	7819	6 CS078969	CS078969 Sequence
37	49.4	8.3	7828	6 AX427809	AX427809 Sequence
38	49.4	8.3	7841	6 CS078964	CS078964 Sequence
39	49.4	8.3	7844	6 CS078966	CS078966 Sequence
40	49.4	8.3	7852	6 CS078967	CS078967 Sequence
41	49.4	8.3	7867	6 AX427804	AX427804 Sequence
42	49.4	8.3	7870	6 AX427801	AX427801 Sequence
43	49.4	8.3	7870	6 AX427805	AX427805 Sequence
44	49.4	8.3	7885	6 AX427806	AX427806 Sequence
45	49.4	8.3	7906	6 AX427802	AX427802 Sequence

ALIGNMENTS

RESULT 1
I36987
LOCUS I36987 382 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5612213.
ACCESSION I36987
VERSION I36987.1 GI:2084947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 382)
AUTHORS Chaf,S.Y.
TITLE Method of selecting mammalian cell lines having improved productivity
JOURNAL Patent: US 5612213-A 1 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..382
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 8.3%; Score 49.4; DB 6; Length 382;
Best Local Similarity 83.6%; Pred. No. 0.0012;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 488 CCGGTGTTCTTGAAGGCGCCTATATAGGGGGGGCGGCTTCCTCATCTCGA 547
Db 197 CCGGTGTTCTTGAAGGCGGCTATAAAGGGGGTGGGGCGGCTTCCTCATCTCTT 256
QY 548 CCGCGTC 554
Db 257 CCGCATC 263
RESULT 2
I02395
LOCUS I02395 560 bp ss-DNA linear PAT 18-MAY-1993
DEFINITION Sequence 1 from Patent US 4510245.
ACCESSION I02395
VERSION I02395.1 GI:268039
KEYWORDS